



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/667,569

Source: C1P0

Date Processed by STIC: 5 - 7-01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE SEE BELOW**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Sequence Listing Error Summary

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## ERROR DETECTED    SUGGESTED    CORRECTION

SERIAL NUMBER: 07/1667,569

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- |    |                                      |   |
|----|--------------------------------------|---|
| 1  | ____ Wrapped Nucleic                 | The number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".   |
| 2  | ____ Wrapped Aminos                  | The amino acid number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".  |
| 3  | ____ Incorrect Line Length           | The rules require that a line not exceed 72 characters in length. This includes spaces.   |
| 4  | ____ Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.   |
| 5  | ____ Non-ASCII                       | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.<br>Please ensure your subsequent submission is saved in ASCII text so that it can be processed.   |
| 6  | ____ Variable Length                 | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.<br>As per the rules, each n or Xaa can only represent a single residue.<br>Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.   |
| 7  | ____ PatentIn ver. 2.0 "bug"         | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.          |
| 8  | ____ Skipped Sequences (OLD RULES)   | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:<br><b>(2) INFORMATION FOR SEQ ID NO:X:</b><br>(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:<br>This sequence is intentionally skipped<br><br>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9  | ____ Skipped Sequences (NEW RULES)   | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:<br><210> sequence id number<br><400> sequence id number<br>000   |
| 10 | ✓ Use of n's or Xaa's (NEW RULES)    | Use of n's and/or Xaa's have been detected in the Sequence Listing<br>Use of <220> to <223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents  |
| 11 | ____ Use of "Artificial" (NEW RULES) | Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules<br>Valid response is Artificial Sequence.   |
| 12 | ____ Use of <220>Feature (NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.<br>Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"<br>Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec 1.823 of new Rules)   |
| 13 | ____ PatentIn ver 2.0 "bug"          | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing)<br>Instead, please use "File Manager" or any other means to copy file to floppy disk   |

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/667,569

DATE: 05/07/2001  
TIME: 17:56:42

Input Set : A:\sequence.txt  
Output Set: N:\CRF3\05072001\I667569.raw

3 <110> APPLICANT: Yocum, R. et al.  
 5 <120> TITLE OF INVENTION: METHODS AND MICROORGANISMS FOR PRODUCTION OF  
 6 PANTO-COMPOUNDS  
 8 <130> FILE REFERENCE: BGI-141CP  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/667,569  
 C--> 11 <141> CURRENT FILING DATE: 2000-09-21  
 13 <150> PRIOR APPLICATION NUMBER: USSN 09/400,494  
 14 <151> PRIOR FILING DATE: 1999-09-21  
 16 <150> PRIOR APPLICATION NUMBER: USSN 60/210,072  
 17 <151> PRIOR FILING DATE: 2000-06-07  
 19 <150> PRIOR APPLICATION NUMBER: USSN 60/221,836  
 20 <151> PRIOR FILING DATE: 2000-07-28  
 W--> 22 <150> PRIOR APPLICATION NO: USSN 60/221,838 → Duplicate application number.  
 Does Not Comply  
 Corrected Diskette Needed  
 pp. 1, 6  
 23 <151> PRIOR FILING DATE: 2000-08-24  
 25 <160> NUMBER OF SEQ ID NOS: 94  
 27 <170> SOFTWARE: PatentIn Ver. 2.0  
 29 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 311  
 31 <212> TYPE: PRT  
 32 <213> ORGANISM: Haemophilus influenzae  
 34 <400> SEQUENCE: 1  
 35 Met Glu Phe Ser Thr Gln Gln Thr Pro Phe Leu Ser Phe Asn Arg Glu  
 36 1 5 10 15  
 38 Gln Trp Ala Glu Leu Arg Lys Ser Val Pro Leu Lys Leu Thr Glu Gln  
 39 20 25 30  
 41 Asp Leu Lys Pro Leu Leu Gly Phe Asn Glu Asp Leu Ser Leu Asp Glu  
 42 35 40 45  
 44 Val Ser Thr Ile Tyr Leu Pro Leu Thr Arg Leu Ile Asn Tyr Tyr Ile  
 45 50 55 60  
 47 Asp Glu Asn Leu His Arg Gln Thr Val Leu His Arg Phe Leu Gly Arg  
 48 65 70 75 80  
 50 Asn Asn Ala Lys Thr Pro Tyr Ile Ile Ser Ile Ala Gly Ser Val Ala  
 51 85 90 95  
 53 Val Gly Lys Ser Thr Ser Ala Arg Ile Leu Gln Ser Leu Leu Ser His  
 54 100 105 110  
 56 Trp Pro Thr Glu Arg Lys Val Asp Leu Ile Thr Thr Asp Gly Phe Leu  
 57 115 120 125  
 59 Tyr Pro Leu Asn Lys Leu Lys Gln Asp Asn Leu Leu Gln Lys Lys Gly  
 60 130 135 140  
 62 Phe Pro Val Ser Tyr Asp Thr Pro Lys Leu Ile Arg Phe Leu Ala Asp  
 63 145 150 155 160  
 65 Val Iys Ser Gly Lys Ser Asn Val Thr Ala Pro Ile Tyr Ser His Leu  
 66 165 170 175  
 68 Thr Tyr Asp Ile Ile Pro Asp Lys Phe Asp Val Val Asp Lys Pro Asp  
 69 180 185 190  
 71 Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr Gly Asn Asn Lys  
 72 195 200 205

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/667,569

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TIME: 17:56:42

Input Set : A:\sequence.txt  
Output Set N:\CRF3\05072001\I667569.raw

74 Thr Asp Gln Thr Phe Val Ser Asp Phe Val Asp Phe Ser Ile Tyr Val  
75 210 215 220  
77 Asp Ala Glu Glu Lys Leu Leu Lys Glu Trp Tyr Ile Lys Arg Phe Leu  
78 225 230 235 240  
80 Lys Phe Arg Glu Ser Ala Phe Asn Asp Pro Asn Ser Tyr Phe Lys His  
81 245 250 255  
83 Tyr Ala Ser Leu Ser Lys Glu Glu Ala Ile Ala Thr Ala Ser Lys Ile  
84 260 265 270  
86 Trp Asp Glu Ile Asn Gly Leu Asn Leu Asn Gln Asn Ile Leu Pro Thr  
87 275 280 285  
89 Arg Glu Arg Ala Asn Leu Ile Leu Lys Lys Gly His Asn His Gln Val  
90 290 295 300  
92 Glu Leu Ile Lys Leu Arg Lys  
93 305 310  
96 <210> SEQ ID NO 2  
97 <211> LENGTH 316  
98 <212> TYPE: PRT  
99 <213> ORGANISM Escherichia coli  
101 <400> SEQUENCE 2  
102 Met Ser Ile Lys Glu Gln Thr Leu Met Thr Pro Tyr Leu Gln Phe Asp  
103 1 5 10 15  
105 Arg Asn Gln Trp Ala Ala Leu Arg Asp Ser Val Pro Met Thr Leu Ser  
106 20 25 30  
108 Glu Asp Glu Ile Ala Arg Leu Lys Gly Ile Asn Glu Asp Leu Ser Leu  
109 35 40 45  
111 Glu Glu Val Ala Glu Ile Tyr Leu Pro Leu Ser Arg Leu Leu Asn Phe  
112 50 55 60  
114 Tyr Ile Ser Ser Asn Leu Arg Arg Gln Ala Val Leu Glu Gln Phe Leu  
115 65 70 75 80  
117 Gly Thr Asn Gly Gln Arg Ile Pro Tyr Ile Ile Ser Ile Ala Gly Ser  
118 85 90 95  
120 Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala Leu Leu  
121 100 105 110  
123 Ser Arg Trp Pro Glu His Arg Arg Val Glu Leu Ile Thr Thr Asp Gly  
124 115 120 125  
126 Phe Leu His Pro Asn Gln Val Leu Lys Glu Arg Gly Leu Met Lys Lys  
127 130 135 140  
129 Lys Gly Phe Pro Glu Ser Tyr Asp Met His Arg Leu Val Lys Phe Val  
130 145 150 155 160  
132 Ser Asp Leu Lys Ser Gly Val Pro Asn Val Thr Ala Pro Val Tyr Ser  
133 165 170 175  
135 His Leu Ile Tyr Asp Val Ile Pro Asp Gly Asp Lys Thr Val Val Gln  
136 180 185 190  
138 Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Ser Gly Met  
139 195 200 205  
141 Asp Tyr Pro His Asp Pro His His Val Phe Val Ser Asp Phe Val Asp  
142 210 215 220  
144 Phe Ser Ile Tyr Val Asp Ala Pro Glu Asp Leu Leu Gln Thr Trp Tyr  
145 225 230 235 240

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/667,569

DATE 05/07/2001  
TIME 17:56:42

Input Set : A:\sequence.txt  
Output Set: N:\CRF3\05072001\I667569.raw

```

147 Ile Asn Arg Phe Leu Lys Phe Arg Glu Gly Ala Phe Thr Asp Pro Asp
148          245          250          255
150 Ser Tyr Phe His Asn Tyr Ala Lys Leu Thr Lys Glu Glu Ala Ile Lys
151          260          265          270
153 Thr Ala Met Thr Leu Trp Lys Glu Ile Asn Trp Leu Asn Leu Lys Gln
154          275          280          285
156 Asn Ile Leu Pro Thr Arg Glu Arg Ala Ser Leu Ile Leu Thr Lys Ser
157          290          295          300
159 Ala Asn His Ala Val Glu Glu Val Arg Leu Arg Lys
160 305          310          315
163 <210> SEQ ID NO: 3
164 <211> LENGTH: 319
165 <212> TYPE: PRT
166 <213> ORGANISM: Bacillus subtilis
168 <400> SEQUENCE 3
169 Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn
170   1          5          10          15
172 Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser
173          20          25          30
175 Glu Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val
176          35          40          45
178 Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Leu Leu His Leu
179          50          55          60
181 His Val Lys Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu
182 65          70          75          80
184 Lys His Pro His Ser Ala Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly
185          85          90          95
187 Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu
188          100         105         110
190 Leu Ser Arg Leu Pro Asp Arg Pro Lys Val Ser Leu Ile Thr Thr Asp
191          115         120         125
193 Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys Lys Asn Met Met Ser
194          130         135         140
196 Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe
197 145          150          155          160
199 Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser Val Lys Ala Pro Val Tyr
200          165         170         175
202 Ser His Leu Thr Tyr Asp Arg Glu Glu Gly Val Phe Glu Val Val Glu
203          180         185         190
205 Gln Ala Asp Ile Val Ile Glu Gly Ile Asn Val Leu Gln Ser Prc
206          195         200         205
208 Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg Ile Phe Val Ser Asp Phe
209 210          215          220
211 Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu Glu Ser Arg Ile Phe Thr
212 225          230          235          240
214 Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn
215          245          250          255
217 Pro Asp Ser Tyr Phe His Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala
218          260          265          270

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,569

DATE: 05/07/2001

TIME: 17:56:42

Input Set : A:\sequence.txt  
 Output Set: N:\CRF3\05072001\I667569.raw

220 Asp Glu Met Ala Ala Ser Ile Trp Glu Ser Val Asn Arg Pro Asn Leu  
 221 275 280 285  
 223 Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg  
 224 290 295 300  
 226 Lys Gly Asp Gly His Lys Val Glu Glu Val Leu Val Arg Arg Val  
 227 305 310 315  
 230 <210> SEQ ID NO: 4  
 231 <211> LENGTH: 312  
 232 <212> TYPE: PRT  
 233 <213> ORGANISM: Mycobacterium leprae  
 235 <400> SEQUENCE: 4  
 236 Met Pro Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Lys  
 237 1 5 10 15  
 239 Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu  
 240 20 25 30  
 242 Glu Leu Ile Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu  
 243 35 40 45  
 245 Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val  
 246 50 55 60  
 248 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu  
 249 65 70 75 80  
 251 Pro Gln Gln Asn Pro Gly Arg Pro Val Pro Phe Ile Ile Gly Val Ala  
 252 85 90 95  
 254 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala  
 255 100 105 110  
 257 Leu Leu Ala Arg Trp Asp His His Thr Arg Val Asp Leu Val Thr Thr  
 258 115 120 125  
 260 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gly Arg Arg Asn Leu Met  
 261 130 135 140  
 263 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg  
 264 145 150 155 160  
 266 Phe Val Thr Ser Val Lys Ser Gly Ala Asp Tyr Ala Cys Ala Pro Val  
 267 165 170 175  
 269 Tyr Ser His Leu Arg Tyr Asp Thr Ile Pro Gly Ala Lys His Val Val  
 270 180 185 190  
 272 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr  
 273 195 200 205  
 275 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val  
 276 210 215 220  
 278 Asp Ala Arg Ile Gln Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu  
 279 225 230 235 240  
 281 Ala Met Arg Gly Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His  
 282 245 250 255  
 284 Tyr Ser Ala Leu Thr Asp Ser Lys Ala Ile Ile Ala Ala Arg Glu Ile  
 285 260 265 270  
 287 Trp Arg Ser Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr  
 288 275 280 285  
 290 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile  
 291 290 295 300

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/667,569

DATE: 05/07/2001  
TIME: 17:56:42

Input Set A:\sequence.txt  
Output Set N:\CRF3\05072001\I667569.raw

293 Asn Arg Leu Arg Leu Arg Lys Leu  
294 305 310  
297 <210> SEQ ID NO: 5  
298 <211> LENGTH: 312  
299 <212> TYPE: PRT  
300 <213> ORGANISM: Mycobacterium tuberculosis  
302 <400> SEQUENCE: 5  
303 Met Ser Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Arg  
304 1 5 10 15  
305 Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu  
306 20 25 30  
307 Glu Leu Val Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu  
308 35 40 45  
309 Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val  
310 50 55 60  
311 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu  
312 65 70 75 80  
313 Pro Gln Gln Asn Pro Asp Arg Pro Val Pro Phe Ile Ile Gly Val Ala  
314 85 90 95  
315 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala  
316 100 105 110  
317 Leu Leu Ala Arg Trp Asp His His Pro Arg Val Asp Leu Val Thr Thr  
318 115 120 125  
319 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gln Arg Arg Asn Leu Met  
320 130 135 140  
321 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg  
322 145 150 155 160  
323 Phe Val Thr Ser Val Lys Ser Gly Ser Asp Tyr Ala Cys Ala Pro Val  
324 165 170 175  
325 Tyr Ser His Leu His Tyr Asp Ile Ile Pro Gly Ala Glu Gln Val Val  
326 180 185 190  
327 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr  
328 195 200 205  
329 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val  
330 210 215 220  
331 Asp Ala Arg Ile Glu Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu  
332 225 230 235 240  
333 Ala Met Arg Thr Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His  
334 245 250 255  
335 Tyr Ala Ala Phe Ser Asp Ser Gln Ala Val Val Ala Ala Arg Glu Ile  
336 260 265 270  
337 Trp Arg Thr Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr  
338 275 280 285  
339 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile  
340 290 295 300  
341 Asn Arg Leu Arg Leu Arg Lys Leu  
342 305 310  
343 <210> SEQ ID NO: 6  
344 <211> LENGTH 329

&lt;210&gt; 45

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: ribosome  
binding site

&lt;400&gt; 45

tttagaaagg aggtgannnn atg

23

&lt;210&gt; 45

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: ribosome  
binding site

&lt;400&gt; 46

tttagaaagg ggtgannnnn atg

23

&lt;210&gt; 47

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: ribosome  
binding site

&lt;400&gt; 47

agaaaaggagg tgannnnnnn atg

23

&lt;210&gt; 48

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: ribosome  
binding site

&lt;400&gt; 48

agaaaaggagg tgannnnnnna tg

22



These sequences also missing the mandatory  
<220> + <223> therefore they lack the "P" in  
the sequence. See this on the ESR.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/667,569

DATE 05/07/2001  
TIME 17:56:43

Input Set : A:\sequence.txt  
Output Set: N:\CRF3\05072001\I667569.raw

L.10 M:270 C: Current Application Number differs, Replaced Application Number  
L.11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L.22 M:288 W: Application Number is Repeated, <150> PRIOR APPLICATION NUMBER  
L.2892 M.258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45  
L.2892 M.258 W: Mandatory Feature missing, <222> not found for SEQ ID#.45  
L.2892 M.341 W: (46) "n" or "Xaa" used, for SEQ ID#:45  
L.2904 M.258 W: Mandatory Feature missing, <221> not found for SEQ ID# 46  
L.2904 M.258 W: Mandatory Feature missing, <222> not found for SEQ ID# 46  
L.2904 M.341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L.2918 M.258 W: Mandatory Feature missing, <221> not found for SEQ ID#:47  
L.2918 M.258 W: Mandatory Feature missing, <222> not found for SEQ ID#:47  
L.2918 M.341 W: (46) "n" or "Xaa" used, for SEQ ID#:47  
L.2930 M.258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48  
L.2930 M.258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48  
L.2930 M.341 W: (46) "n" or "Xaa" used, for SEQ ID#:48  
L.7767 M.258 W: Mandatory Feature missing, <221> not found for SEQ ID#:88  
L.7767 M.258 W: Mandatory Feature missing, <222> not found for SEQ ID#:88  
L.7767 M.341 W: (46) "n" or "Xaa" used, for SEQ ID#:88